

## RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number: 10/518,752  
Source: PST  
Date Processed by STIC: 1-10-05

# *ENTERED*



PCT

## RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/518,752

DATE: 01/10/2005

TIME: 15:26:56

Input Set : A:\PTO.FG.txt

Output Set: N:\CRF4\01102005\J518752.raw

3 <110> APPLICANT: Monsanto Technology, LLC  
 5 <120> TITLE OF INVENTION: THIOESTERASE-RELATED NUCLEIC ACID SEQUENCES AND METHODS OF  
 USE FOR THE

6 PRODUCTION OF PLANTS WITH MODIFIED FATTY ACID COMPOSITION

W--&gt; 7 &lt;130&gt; FILE REFERENCE: 16518.128

C--&gt; 9 &lt;140&gt; CURRENT APPLICATION NUMBER: US/10/518,752

C--&gt; 9 &lt;141&gt; CURRENT FILING DATE: 2004-12-21

9 &lt;160&gt; NUMBER OF SEQ ID NOS: 20

11 &lt;170&gt; SOFTWARE: PatentIn version 3.1

13 &lt;210&gt; SEQ ID NO: 1

14 &lt;211&gt; LENGTH: 4086

15 &lt;212&gt; TYPE: DNA

16 &lt;213&gt; ORGANISM: Glycine max

18 &lt;220&gt; FEATURE:

19 &lt;223&gt; OTHER INFORMATION: soybean FATB genomic clone

21 &lt;400&gt; SEQUENCE: 1

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30	caaaccgct	ttttctgcat	ttctagacta	gacgttctac	cggagaagg	tctcgattct	300
32	tttctctttt	aactttattt	ttaaaataat	aataatgaga	gctggatg	tctgttcgtt	360
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40	attccgagtc	agatctgcgc	cggcttatac	gacgaatttg	ttcttattcg	caacttttcg	600
42	cttgattggc	ttgttttacc	tctggaatct	cacacgtgat	caaataagcc	tgctatttta	660
44	gttgaagtag	aatttgttct	ttatcgga	gaattctatg	gatctgttct	gaaattggag	720
46	ctactgtttc	gagttgctat	tttttttagt	agtattaaga	acaagtttgc	cttttat	780
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72	atgcttattg	acccttttgg	gataggaaaa	attgttcagg	atggtcttgt	gttccgtgaa	1560
74	aacttttcta	ttagatcata	tgagattggt	gctgatcgta	ccgcatctat	agaaacagta	1620
76	atgaaccatt	tgcaagtaag	tccgtcctca	tacaagtga	tctttatgat	cttcagagat	1680

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82 acaggaaact gcacttaatc atgttaaaag tgctgggctt cttgggtgatg gctttgggtc 1860
84 cacgccagaa atgtgcaaaa agaacttgat atgggtgggt actcggatgc aggttgtggt 1920
86 ggaacgctat cctacatggt tagtcatcta gattcaacca ttacatgtga tttgcaatgt 1980
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146 ttattctggc ctctggggag agttttgctt gtgtctgtcc aatcaatcta catatcttta 3780
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154 gctcaattaa agatgcaatt ttcattgtga acacagcata actattattc ttattatttt 4020
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158 gctcag 4086
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162 <211> LENGTH: 104
163 <212> TYPE: DNA
164 <213> ORGANISM: Glycine max
166 <220> FEATURE:
167 <223> OTHER INFORMATION: soybean FATB intron I
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170 caaatctgct attcattcat tcattcctct ttctctctga tcgcaaactg cacctctacg 60

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180 <220> FEATURE:
181 <223> OTHER INFORMATION: soybean FATB intron II
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188 ttgtctgctt tcctcttctc ccttggtttt ttgccttgtc tgatttttcg tttttatttc 180
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198 aaattggagc tactgtttcg agttgctatt ttttttagta gtattaagaa caagtgtgcc 480
200 ttttatttta catttttttc ctttgctttt gccaaaagtt tttatgatca ctctcttctg 540
202 tttgtgatat aactgatgtg ctgtgctggt attatttgtt atttggggtg aagtataatt 600
204 ttttgggtga acttgagca tttttagtcc gattgatttc tcgatatcat ttaaggctaa 660
206 ggttgacctc taccacgcgt ttgcgtttga tgttttttcc attttttttt tatctcatat 720
208 cttttacagt gtttgccat ttgcatttct cttctttatc ccctttctgt ggaagggtggg 780
210 agggaaaatg tatttttttt ttctcttcta acttgcgtat attttgcatg cagcgacct 839
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214 <211> LENGTH: 169
215 <212> TYPE: DNA
216 <213> ORGANISM: Glycine max
218 <220> FEATURE:
219 <223> OTHER INFORMATION: soybean FATB intron III
221 <400> SEQUENCE: 4
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224 agatagggtt gtttatttag aactgtaat tcaatttcac atatagataa tatcattctg 120
226 ttgttacttt tcatactata tttatatcaa ctatttgctt aacaacagg 169
229 <210> SEQ ID NO: 5
230 <211> LENGTH: 525
231 <212> TYPE: DNA
232 <213> ORGANISM: Glycine max
234 <220> FEATURE:
235 <223> OTHER INFORMATION: FATB intron IV
237 <400> SEQUENCE: 5
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242 aattattgag acttaattat gagaaccaa atgctttgga aatttgctct ggatgaaaat 180
244 tgattagata cacaagcttt atacatgatg aactatggga aaccttgtgc aacagagcta 240
246 ttgatctgta caagagatgt agtatagcat taattacatg ttattagata aggtgactta 300
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250 ttaccagtta tatataccct ctgttctggt tgagtactac tagatgtata aagaatgcaa 420
252 ttattctgac ttcttggtgt tgggttgaag ttagataagc tattagtatt attatgggta 480
254 ttctaaatct aattatctga aattgtgtgt ctatatttgc ttcag 525
257 <210> SEQ ID NO: 6

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## RAW SEQUENCE LISTING

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Output Set: N:\CRF4\01102005\J518752.raw

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258 <211> LENGTH: 389
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260 <213> ORGANISM: Glycine max
262 <220> FEATURE:
263 <223> OTHER INFORMATION: FATB intron V
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270 caaaagttat ggaacccttt cttttctctc ttgaagatgc aaatttgtca cgactgaagt      180
272 ttgaggaaat catttgaatt ttgcaatgtt aaaaaagata atgaactaca tattttgcag      240
274 gcaaaaacct ctaattgaac aaactgaaca ttgtatctta gtttatttat cagactttat      300
276 catgtgtact gatgcatcac cttggagctt gtaatgaatt acatattagc attttctgaa      360
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282 <211> LENGTH: 106
283 <212> TYPE: DNA
284 <213> ORGANISM: Glycine max
286 <220> FEATURE:
287 <223> OTHER INFORMATION: FATB intron VI
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298 <213> ORGANISM: Glycine max
300 <220> FEATURE:
301 <223> OTHER INFORMATION: FATB intron VII
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306 actgtccttt gattgtttgc ag      82
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310 <211> LENGTH: 328
311 <212> TYPE: PRT
312 <213> ORGANISM: Glycine max
314 <220> FEATURE:
315 <223> OTHER INFORMATION: soybean FATB enzyme
317 <400> SEQUENCE: 9
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319   1           5           10           15
321 Glu Lys Gln Trp Met Met Leu Asp Trp Lys Pro Arg Arg Pro Asp Met
322           20           25           30
324 Leu Ile Asp Pro Phe Gly Ile Gly Lys Ile Val Gln Asp Gly Leu Val
325           35           40           45
327 Phe Arg Glu Asn Phe Ser Ile Arg Ser Tyr Glu Ile Gly Ala Asp Arg
328   50           55           60
330 Thr Ala Ser Ile Glu Thr Val Met Asn His Leu Gln Glu Thr Ala Leu
331 65           70           75           80
333 Asn His Val Lys Ser Ala Gly Leu Leu Gly Asp Gly Phe Gly Ser Thr

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339	Val	Val	Val	Glu	Arg	Tyr	Pro	Thr	Trp	Gly	Asp	Ile	Val	Gln	Val	Asp
340			115					120					125			
342	Thr	Trp	Val	Ser	Gly	Ser	Gly	Lys	Asn	Gly	Met	Arg	Arg	Asp	Trp	Leu
343		130					135					140				
345	Leu	Arg	Asp	Ser	Lys	Thr	Gly	Glu	Ile	Leu	Thr	Arg	Ala	Ser	Ser	Val
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348	Trp	Val	Met	Met	Asn	Lys	Leu	Thr	Arg	Arg	Leu	Ser	Lys	Ile	Pro	Glu
349				165					170					175		
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352			180						185				190			
354	Leu	Glu	Glu	Asp	Asn	Arg	Lys	Leu	Thr	Lys	Leu	Asp	Asp	Asn	Thr	Ala
355		195					200					205				
357	Asp	Tyr	Ile	Arg	Thr	Gly	Leu	Ser	Pro	Arg	Trp	Ser	Asp	Leu	Asp	Ile
358		210				215					220					
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361	225			230						235				240		
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364			245						250				255			
366	Glu	Tyr	Arg	Arg	Glu	Cys	Gly	Arg	Asp	Ser	Val	Leu	Asp	Ser	Leu	Thr
367		260						265				270				
369	Ala	Val	Ser	Gly	Ala	Asp	Met	Gly	Asn	Leu	Ala	His	Ser	Gly	His	Val
370		275					280				285					
373	Glu	Cys	Lys	His	Leu	Leu	Arg	Leu	Glu	Asn	Gly	Ala	Glu	Ile	Val	Arg
374		290				295					300					
376	Gly	Arg	Thr	Glu	Trp	Arg	Pro	Lys	Pro	Val	Asn	Asn	Phe	Gly	Val	Val
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396	tgctattcat	tcattcattc	ctctttctct	ctgatcgcaa	actgcacctc	tacgctccac		180								
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RAW SEQUENCE LISTING ERROR SUMMARY  
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Invalid <213> Response:

Use of "Artificial" only as "<213> Organism" response is incomplete,  
per 1.823(b) of New Sequence Rules. Valid response is Artificial Sequence.

Seq#:11,12,13,14,15,16,17,18,19

## VERIFICATION SUMMARY

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Input Set : A:\PTO.FG.txt

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L:7 M:283 W: Missing Blank Line separator, <130> field identifier  
L:9 M:270 C: Current Application Number differs, Replaced Current Application No  
L:9 M:271 C: Current Filing Date differs, Replaced Current Filing Date